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The TNF family ligands identified to date, with the exception of lymphotoxin- α , are type II transmembrane proteins, whose C-terminus is extracellular. In contrast, most receptors in the TNF receptor (TNFR) family identified to date are type I transmembrane proteins. In both the TNF ligand and receptor families, however, homology identified between family members has been found mainly in the extracellular domain ("ECD"). Several of the TNF family cytokines, including TNF- α , Apo-1 ligand and CD40 ligand, are cleaved proteolytically at the cell surface; the resulting protein in each case typically forms a homotrimeric molecule that functions as a soluble cytokine. TNF receptor family proteins are also usually cleaved proteolytically to release soluble receptor ECDs that can function as inhibitors of the cognate cytokines.

Recently, other members of the TNFR family have been identified. Such newly identified members of the TNFR family include CAR1, HVEM and osteoprotegerin (OPG) [Brojatsch et al., Cell, 87:845-855 (1996); Montgomery et al., Cell, 87:427-436 (1996); Marsters et al., J. Biol. Chem., 272:14029-14032 (1997); Simonet et al., Cell, 89:309-319 (1997)]. Unlike other known TNFR-like molecules, Simonet et al., supra, report that OPG contains no hydrophobic transmembrane-spanning sequence.

Moreover, a new member of the TNF/NGF receptor family has been identified in mouse, a receptor referred to as "GITR" for "glucocorticoid-induced tumor necrosis factor receptor family-related gene" [Nocentini et al., Proc. Natl. Acad. Sci. USA 94:6216-6221 (1997)]. The mouse GITR receptor is a 228 amino acid type I transmembrane protein that is expressed in normal mouse T lymphocytes from thymus, spleen and lymph nodes. Expression of the mouse GITR receptor was induced in T lymphocytes upon activation with anti-CD3 antibodies, Con A or phorbol 12-myristate 13-acetate. It was speculated by the authors that the mouse GITR receptor was involved in the regulation of T cell receptor-mediated cell death.

In Marsters et al., Curr. Biol., 6:750 (1996), investigators describe a full length native sequence human polypeptide, called Apo-3, which exhibits similarity to the TNFR family in its extracellular cysteine-rich repeats and resembles TNFR1 and CD95 in that it contains a cytoplasmic death domain sequence [see also Marsters et al., Curr. Biol., 6:1669 (1996)]. Apo-3 has also been referred to by other investigators as DR3, wsl-1 and TRAMP [Chinnaiyan et al., Science, 274:990 (1996); Kitson et al., Nature, 384:372 (1996); Bodmer et al., Immunity, 6:79 (1997)].

Pan et al. have disclosed another TNF receptor family member referred to as "DR4" [Pan et al., Science, 276:111-113 (1997)]. The DR4 was reported to contain a cytoplasmic death domain capable of engaging the cell suicide apparatus. Pan et al. disclose that DR4 is believed to be a receptor for the ligand known as Apo-2 ligand or TRAIL.

In Sheridan et al., Science, 277:818-821 (1997) and Pan et al., Science, 277:815-818 (1997), another molecule believed to be a receptor for the Apo-2 ligand (TRAIL) is described. That molecule is referred to as DR5 (it has also been alternatively referred to as Apo-2). Like DR4, DR5 is reported to contain a cytoplasmic death domain and be capable of signaling apoptosis.

In Sheridan et al., supra, a receptor called DcR1 (or alternatively, Apo-2DcR) is disclosed as being a potential decoy receptor for Apo-2 ligand (TRAIL). Sheridan et al. report that DcR1 can inhibit Apo-2 ligand function *in vitro*. See also, Pan et al., supra, for disclosure on the decoy receptor referred to as TRID.

For a review of the TNF family of cytokines and their receptors, see Gruss and Dower, supra.

As presently understood, the cell death program contains at least three important elements - activators,

inhibitors, and effectors; in *C. elegans*, these elements are encoded respectively by three genes, *Ced-4*, *Ced-9* and *Ced-3* [Steller, *Science*, 267:1445 (1995); Chinnaiyan et al., *Science*, 275:1122-1126 (1997); Wang et al., *Cell*, 90:1-20 (1997)]. Two of the TNFR family members, TNFR1 and Fas/Apo1 (CD95), can activate apoptotic cell death [Chinnaiyan and Dixit, *Current Biology*, 6:555-562 (1996); Fraser and Evan, *Cell*, 85:781-784 (1996)]. TNFR1 is also known to mediate activation of the transcription factor, NF- κ B [Tartaglia et al., *Cell*, 74:845-853 (1993); Hsu et al., *Cell*, 84:299-308 (1996)]. In addition to some ECD homology, these two receptors share homology in their intracellular domain (ICD) in an oligomerization interface known as the death domain [Tartaglia et al., *supra*; Nagata, *Cell*, 88:355 (1997)]. Death domains are also found in several metazoan proteins that regulate apoptosis, namely, the Drosophila protein, Reaper, and the mammalian proteins referred to as FADD/MORT1, TRADD, and RIP [Cleveland and Ihle, *Cell*, 81:479-482 (1995)].

Upon ligand binding and receptor clustering, TNFR1 and CD95 are believed to recruit FADD into a death-inducing signalling complex. CD95 purportedly binds FADD directly, while TNFR1 binds FADD indirectly via TRADD [Chinnaiyan et al., *Cell*, 81:505-512 (1995); Boldin et al., *J. Biol. Chem.*, 270:387-391 (1995); Hsu et al., *supra*; Chinnaiyan et al., *J. Biol. Chem.*, 271:4961-4965 (1996)]. It has been reported that FADD serves as an adaptor protein which recruits the *Ced-3*-related protease, MACH α /FLICE (caspase 8), into the death signalling complex [Boldin et al., *Cell*, 85:803-815 (1996); Muzio et al., *Cell*, 85:817-827 (1996)]. MACH α /FLICE appears to be the trigger that sets off a cascade of apoptotic proteases, including the interleukin-1 β converting enzyme (ICE) and CPP32/Yama, which may execute some critical aspects of the cell death programme [Fraser and Evan, *supra*].

It was recently disclosed that programmed cell death involves the activity of members of a family of cysteine proteases related to the *C. elegans* cell death gene, *ced-3*, and to the mammalian IL-1-converting enzyme, ICE. The activity of the ICE and CPP32/Yama proteases can be inhibited by the product of the cowpox virus gene, *crmA* [Ray et al., *Cell*, 69:597-604 (1992); Tewari et al., *Cell*, 81:801-809 (1995)]. Recent studies show that CrmA can inhibit TNFR1- and CD95-induced cell death [Enari et al., *Nature*, 375:78-81 (1995); Tewari et al., *J. Biol. Chem.*, 270:3255-3260 (1995)].

As reviewed recently by Tewari et al., TNFR1, TNFR2 and CD40 modulate the expression of proinflammatory and costimulatory cytokines, cytokine receptors, and cell adhesion molecules through activation of the transcription factor, NF- κ B [Tewari et al., *Curr. Op. Genet. Develop.*, 6:39-44 (1996)]. NF- κ B is the prototype of a family of dimeric transcription factors whose subunits contain conserved Rel regions [Verma et al., *Genes Develop.*, 9:2723-2735 (1996); Baldwin, *Ann. Rev. Immunol.*, 14:649-681 (1996)]. In its latent form, NF- κ B is complexed with members of the I κ B inhibitor family; upon inactivation of the I κ B in response to certain stimuli, released NF- κ B translocates to the nucleus where it binds to specific DNA sequences and activates gene transcription.

PRO382

Proteases are enzymatic proteins which are involved in a large number of very important biological processes in mammalian and non-mammalian organisms. Numerous different protease enzymes from a variety of different mammalian and non-mammalian organisms have been both identified and characterized, including the serine proteases which exhibit specific activity toward various serine-containing proteins. The mammalian

protease enzymes play important roles in biological processes such as, for example, protein digestion, activation, inactivation, or modulation of peptide hormone activity, and alteration of the physical properties of proteins and enzymes.

In light of the important physiological roles played by protease enzymes, efforts are currently being undertaken by both industry and academia to identify new, native protease homologs. Many of these efforts are focused on the screening of mammalian recombinant DNA libraries to identify the coding sequences for novel membrane-bound receptor proteins. Examples of screening methods and techniques are described in the literature [see, for example, Klein et al., *Proc. Natl. Acad. Sci.*, **93**:7108-7113 (1996); U.S. Patent No. 5,536,637]. We herein describe the identification of novel polypeptides having homology to serine protease enzymes, designated herein as PRO382 polypeptides.

11. **PRO545**

The ADAM (A Disintegrin And Metalloprotease) family of proteins of which meltrin is a member may have an important role in cell interactions and in modulating cellular responses. [see, for example, Gilpin et al., *J. Biol. Chem.*, **273**(1):157-166 (1998)]. The ADAM proteins have been implicated in carcinogenesis. Meltrin- α (ADAM12) is a myoblast gene product reported to be required for cell fusion. [Harris et al., *J. Cell. Biochem.*, **67**(1):136-142 (1997); Yagami-Hiromasa et al., *Nature*, **377**:652-656 (1995)]. The meltrins contain disintegrin and metalloprotease domains and are implicated in cell adhesive events involved in development, through the integrin-binding disintegrin domain, but also have an anti-adhesive function through a zinc-dependent metalloprotease domain. [Alfandari et al., *Devel. Biol.*, **182**(2):314-330 (1997)]. Given the medical importance of cell fusion and modulation of cellular responses in carcinogenesis and other disease mechanisms, efforts are currently being undertaken to identify new, native proteins which are involved in cell fusion and modulation of cellular responses. We describe herein the identification of a novel polypeptide which has homology to meltrin, designated herein as PRO545.

12. **PRO617**

CD24 is a protein that is associated with the cell surface of a variety of different cells of the mammalian immune system, including for example, neutrophils, monocytes and some lymphocytes, for example, B lymphocytes. CD24 has been shown to be a ligand for the platelet-associated surface glycoprotein P-selectin (also known as granule membrane protein-140 or GMP-140), a glycoprotein that is constitutively synthesized in both platelets and endothelial cells and becomes exposed on the surface of platelets when those cells become activated. In this way, P-selectin mediates the calcium-dependent adhesion of activated platelets and endothelial cells to the various cells of the immune system that express one or more ligands for the P-selectin molecule, particularly CD24. This mechanism allows for recruitment of immune system cells to locations where they are most needed, for example, sites of injury. Thus, there is substantial interest in identifying novel polypeptides that exhibit homology to the cell surface antigens of the immune system cells. We herein describe the identification and characterization of a novel polypeptide having homology to the CD24 protein, wherein that novel polypeptide is herein designated PRO617.